

Resource Summary Report

Generated by [RRID](#) on Sep 11, 2026

BETASEQ

RRID:SCR_006401

Type: Tool

Proper Citation

BETASEQ (RRID:SCR_006401)

Resource Information

URL: <http://www.unc.edu/~yunmli/betaseq/>

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Description: Software to control Type-I error inflation in partially sequenced data for rare variant association testing. It is typically used to combine sequence and genotype data for the two stage design, in which individuals sequenced in stage one for variant detection are solely or predominantly cases then in stage two the discovered variants are genotyped in the remaining individuals. BETASEQ can work with any existing rare variant association methods that use genotypes or imputed genotypes as input.

Abbreviations: BETASEQ

Resource Type: software resource

Defining Citation: [PMID:24336643](#)

Keywords: variant association testing, variant association, variant

Availability: Free, Public

Resource Name: BETASEQ

Resource ID: SCR_006401

Alternate IDs: OMICS_02213

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T132553+0000

Ratings and Alerts

No rating or validation information has been found for BETASEQ.

No alerts have been found for BETASEQ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.